

(A)

Wed Nov 21 09:18:30 2001 [BLASTN 2.2.1 [Jul-12-2001], NCBI]
Repeats masked (summary below)
/home/ruby/va/Molbio/carpanda/tempblast/ss.DNA59842 (1141 bp)

| Sequences producing High-scoring Segment Pairs: | Frame | Score | Match |
|---|-------|-------|-------|
| Pct E-val | | | |
| 1 P_AAC58384 Human PRO1153 nucleotide sequence SEQ ID | + | 1141 | 1141 |
| 100 0.0 | | | |
| 2 P_AAZ65081 Membrane-bound protein PRO1153 encoding | + | 1141 | 1141 |
| 100 0.0 | | | |
| 3 P_AAF44227 Human PRO1153 (UNQ583) nucleotide sequen | + | 1141 | 1141 |
| 100 0.0 | | | |
| 4 BC009558 Homo sapiens, clone IMAGE:3899550, mRNA, | + | 1137 | 1140 |
| 100 0.0 | | | |
| 5 P_AAD12571 Human protein having hydrophobic domain | + | 1133 | 1136 |
| 100 0.0 | | | |
| 6 AX191504 Sequence 26 from Patent WO0149728. DNA, | + | 1133 | 1136 |
| 100 0.0 | | | |

>1 P_AAC58384 Human PRO1153 nucleotide sequence SEQ ID NO:48. (1141 bp)
[1 seg]
Score = 1141 (2262 bits), Expect = 0.0
Identities = 1141/1141 (100%), at 1,1-1141,1141, Strand +/-

ss.DNA59842 1
GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

P_AAC58384 1
GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61
GGCCCGACCCCGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGC

P_AAC58384 61
GGCCCGACCCCGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGC

ss.DNA59842 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

P_AAC58384 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

P_AAC58384 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

P_AAC58384 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

BLAST RESULTS A-1

```

ss.DNA59842   301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC
*****
P_AAC58384    301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842   361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC
*****
P_AAC58384    361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842   421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT
*****
P_AAC58384    421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

ss.DNA59842   481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG
*****
P_AAC58384    481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842   541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC
*****
P_AAC58384    541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842   601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC
*****
P_AAC58384    601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842   661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGAT
*****
P_AAC58384    661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGAT

ss.DNA59842   721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT
*****
P_AAC58384    721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

ss.DNA59842   781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC
*****
P_AAC58384    781

```

BLAST RESULTS A-2

CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841

AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT

P_AAC58384 841

AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT

ss.DNA59842 901

ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTACAGTGCCTGTT

P_AAC58384 901

ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTACAGTGCCTGTT

ss.DNA59842 961

TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

P_AAC58384 961

TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

ss.DNA59842 1021

CCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

P_AAC58384 1021

CCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081

CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

P_AAC58384 1081

CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

ss.DNA59842 1141 A

*

P_AAC58384 1141 A

>2 P_AAZ65081 Membrane-bound protein PRO1153 encoding cDNA. (1141 bp) [1
seg]

Score = 1141 (2262 bits), Expect = 0.0

Identities = 1141/1141 (100%), at 1,1-1141,1141, Strand +/+

ss.DNA59842 1

GGGCTGGGCCCCGCCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

P_AAZ65081 1

GGGCTGGGCCCCGCCGCAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61

GGCCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

P_AAZ65081 61

GGCCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

ss.DNA59842 121

BLAST RESULTS A-3

BLAST RESULTS A-4

GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

P_AAZ65081 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

P_AAZ65081 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

P_AAZ65081 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842 301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

P_AAZ65081 301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

P_AAZ65081 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGAT

P_AAZ65081 421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGGAAGGCCAGGAGAT

ss.DNA59842 481
TCCAATGACAGGCATCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

P_AAZ65081 481
TCCAATGACAGGCATCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

P_AAZ65081 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

P_AAZ65081 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

P_AAZ65081 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

ss.DNA59842 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

P_AAZ65081 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

ss.DNA59842 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

P_AAZ65081 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGAATT

P_AAZ65081 841
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGAATT

ss.DNA59842 901
ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

P_AAZ65081 901
ATGGGCTATTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

P_AAZ65081 961
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

ss.DNA59842 1021
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

P_AAZ65081 1021
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081
CTCTCTGGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

P_AAZ65081 1081
CTCTCTGGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

ss.DNA59842 1141 A

P_AAZ65081 1141 A

BLAST RESULTS A-5

BLAST RESULTS A-10

>3 P_AAF44227 Human PRO1153 (UNQ583) nucleotide sequence SEQ ID NO:350.
(1141 bp) [1 seg]
Score = 1141 (2262 bits), Expect = 0.0
Identities = 1141/1141 (100%), at 1,1-1141,1141, Strand +/+

ss.DNA59842 1
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

P_AAF44227 1
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61
GGCCCGACCCCGGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGC

P_AAF44227 61
GGCCCGACCCCGGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGC

ss.DNA59842 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

P_AAF44227 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

P_AAF44227 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

P_AAF44227 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842 301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

P_AAF44227 301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

P_AAF44227 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGAT

P_AAF44227 421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGAT

```

ss.DNA59842 481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAGCTGG
*****
P_AAF44227 481
TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAGCTGG

ss.DNA59842 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCCTGCTCCCCAATATCC
*****
P_AAF44227 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCCTGCTCCCCAATATCC

ss.DNA59842 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC
*****
P_AAF44227 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT
*****
P_AAF44227 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

ss.DNA59842 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT
*****
P_AAF44227 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

ss.DNA59842 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC
*****
P_AAF44227 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGAATT
*****
P_AAF44227 841
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGGAATT

ss.DNA59842 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTACAGTGCCTGTT
*****
P_AAF44227 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTACAGTGCCTGTT

ss.DNA59842 961
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT
*****
P_AAF44227 961

```

BLAST RESULTS A-7

BLAST RESULTS A-9

```
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT
ss.DNA59842 1021
CCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC
*****
P_AAF44227 1021
CCCCTCTGGGCTGGGGTGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC
ss.DNA59842 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA
*****
P_AAF44227 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA
ss.DNA59842 1141 A
*
P_AAF44227 1141 A
>4 BC009558 Homo sapiens, clone IMAGE:3899550, mRNA, partial cds. (1156
bp) [1 seg]
Score = 1137 (2254 bits), Expect = 0.0
Identities = 1140/1141 (99%), at 1,5-1141,1145, Strand +/-
ss.DNA59842 1
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA
*****
BC009558 5
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA
ss.DNA59842 61
GGCCCGACCCCGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC
*****
BC009558 65
GGCCCGACCCCGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC
ss.DNA59842 121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA
*****
BC009558 125
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA
ss.DNA59842 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT
*****
BC009558 185
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT
ss.DNA59842 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTAAGTCTGCAGGGACCTGACCTTGCTTAT
*****
BC009558 245
CACCTTCTGCTGCGGGACCTGCTACCATCGGTAAGTCTGCAGGGACCTGACCTTGCTTAT
ss.DNA59842 301
```


CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

BC009558 305

CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361

CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCAACCATCTGCTGCTTCCTCTGTTC

BC009558 365

CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCAACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421

CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

BC009558 425

CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

ss.DNA59842 481

TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

BC009558 485

TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541

CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

BC009558 545

CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842 601

ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

BC009558 605

ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

ss.DNA59842 661

ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCTTCAGTGAT

BC009558 665

ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCTTCAGTGAT

ss.DNA59842 721

GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

BC009558 725

GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

ss.DNA59842 781

CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

BC009558 785

CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

BLAST RESULTS A-9

ss.DNA59842 841
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTTGGGGGGAGGGCTTGGAATT

BC009558 845
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTTGGGGGGAGGGCTTGGAATT

ss.DNA59842 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

BC009558 905
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

BC009558 965
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

ss.DNA59842 1021
CCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

BC009558 1025
CCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

BC009558 1085
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGACAAA

ss.DNA59842 1141 A

*
BC009558 1145 A

>5 P_AAD12571 Human protein having hydrophobic domain encoding cDNA
clone HP10764. (1372 bp) [1 seg]
Score = 1133 (2246 bits), Expect = 0.0
Identities = 1136/1137 (99%), at 1,236-1137,1372, Strand +/-

ss.DNA59842 1
GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

P_AAD12571 236
GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842 61
GGCCCCACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

P_AAD12571 296
GGCCCCACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

ss.DNA59842 121
GCCGCTCACC GCAATCGCTCTGTTGGTGTCTGGGGGCTCCCCTGGTGTGGCCGGCGAGGA

P_AAD12571 356
GCCGCTCACC GCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842 181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

P_AAD12571 416
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842 241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

P_AAD12571 476
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842 301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

P_AAD12571 536
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842 361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

P_AAD12571 596
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842 421
CTGTTGCTACCTGTACCGCCGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

P_AAD12571 656
CTGTTGCTACCTGTACCGCCGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

ss.DNA59842 481
TCCAATGACAGGCATCCCAAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

P_AAD12571 716
TCCAATGACAGGCATCCCAAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG

ss.DNA59842 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCC

P_AAD12571 776
CCCTGCACCCCCACAGCCTGGCTTCATATACCCACCTAGTGGTCCTGCTCCCCAATATCC

ss.DNA59842 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

P_AAD12571 836
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACC

BLAST RESULTS A-11

ss.DNA59842 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

P_AAD12571 896
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

ss.DNA59842 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

P_AAD12571 956
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

ss.DNA59842 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

P_AAD12571 1016
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

ss.DNA59842 841
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT

P_AAD12571 1076
AGGGAAGTGGAACAGGAGCTGAACTAGAACTATGAGGGGTGGGGGGAGGGCTTGAATT

ss.DNA59842 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

P_AAD12571 1136
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

ss.DNA59842 961
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

P_AAD12571 1196
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

ss.DNA59842 1021
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

P_AAD12571 1256
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

ss.DNA59842 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

P_AAD12571 1316
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

>6 AX191504 Sequence 26 from Patent WO0149728. DNA, PAT 15-AUG-2001
(1372 bp) [1 seg]
Score = 1133 (2246 bits), Expect = 0.0
Identities = 1136/1137 (99%), at 1,236-1137,1372, Strand +/-

BLAST RESULTS A-12

```

ss.DNA59842      1
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA
*****
AX191504      236
GGGCTGGGCCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGA

ss.DNA59842      61
GGCCCCGACCCCGGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC
*****
AX191504      296
GGCCCCGACCCCGGCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGC

ss.DNA59842      121
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA
*****
AX191504      356
GCCGCTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCTGGTGCTGGCCGGCGAGGA

ss.DNA59842      181
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT
*****
AX191504      416
CTGCCTGTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTT

ss.DNA59842      241
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT
*****
AX191504      476
CACCTTCTGCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTAT

ss.DNA59842      301
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC
*****
AX191504      536
CACCGAGAGGCAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGC

ss.DNA59842      361
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC
*****
AX191504      596
CTCAGCTGTGATCCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTC

ss.DNA59842      421
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT
*****
AX191504      656
CTGTTGCTACCTGTACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGAT

ss.DNA59842      481
TCCAATGACAGGCATCCCAGTGCCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG
*****
AX191504      716

```

BLAST RESULTS A-13

BLAST RESULTS A-H

TCCAATGACAGGCATCCCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGG
ss.DNA59842 541
CCCTGCACCCCCACAGCCTGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCC

AX191504 776
CCCTGCACCCCCACAGCCTGGCTTCATATACCCACCTAGTGGTCTGCTCCCCAATATCC
ss.DNA59842 601
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCCTGCAGCTCCTCCTCCCTATATGCCACC

AX191504 836
ACTCTACCCAGCTGGGCCCCCAGTCTACAACCCCTGCAGCTCCTCCTCCCTATATGCCACC
ss.DNA59842 661
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT

AX191504 896
ACAGCCCTCTTACCCGGGAGCCTGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGAT
ss.DNA59842 721
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT

AX191504 956
GCCAACCTTGGGAGATGCCCTCATCCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGT
ss.DNA59842 781
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC

AX191504 1016
CCTCCAGCCACCAGGCCCCAGACCAAGCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCC
ss.DNA59842 841
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTTGGGGGGAGGGCTTGAATT

AX191504 1076
AGGGAAGTGGAAACAGGAGCTGAACTAGAACTATGAGGGGTTGGGGGGAGGGCTTGAATT
ss.DNA59842 901
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT

AX191504 1136
ATGGGCTATTTTTACTGGGGGCAAGGGAGGGAGATGACAGCCTGGGTCACAGTGCCTGTT
ss.DNA59842 961
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT

AX191504 1196
TTCAAATAGTCCCTCTGCTCCCAAGATCCCAGCCAGGAAGGCTGGGGCCCTACTGTTTGT
ss.DNA59842 1021
CCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGGCAGTAGCCCTC

AX191504 1256
CCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGTTCCGTCAGCAGCTGSCAGTAGCCCTC

ss.DNA59842 1081
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

AX191504 1316
CTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTGCTAGATTAAAGCTGTAAAGAC

BLAST RESULTS A-15

(B)

BLAST RESULTS B-1

Wed Nov 21 09:32:36 2001 [BLASTP 2.2.1 [Jul-12-2001], NCBI]
/home/ruby/va/Molbio/carpenda/tempblast/pl.DNA59842.nc (197 aa)

| Sequences producing High-scoring Segment Pairs: | | Score | Match | Pct | E-val |
|---|--|-------|-------|-----|-------|
| 1 | P_AAB65258 Human PRO1153 (UNQ583) protein sequence S | 1118 | 197 | 100 | e-121 |
| 2 | P_AAG81325 Human AFP protein sequence SEQ ID NO:168 | 1118 | 197 | 100 | e-121 |
| 3 | P_AAY66735 Membrane-bound protein PRO1153 - Homo sap | 1118 | 197 | 100 | e-121 |
| 4 | P_AAB24074 Human PRO1153 protein sequence SEQ ID NO: | 1118 | 197 | 100 | e-121 |
| 5 | CAC38575.1 unnamed protein product - Homo sapiens | 1118 | 197 | 100 | e-121 |
| 6 | P_AAE06576 Human protein having hydrophobic domain, | 1114 | 196 | 99 | e-121 |
| 7 | CAC51150.1 unnamed protein product - Homo sapiens | 1114 | 196 | 99 | e-121 |

>1 P_AAB65258 Human PRO1153 (UNQ583) protein sequence SEQ ID NO:351 - Homo (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121

Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAB65258       1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR

DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ
                  *****
P_AAB65258     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAB65258    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc    181 PAAPPPYMPPQPSYPGA
                  *****
P_AAB65258    181 PAAPPPYMPPQPSYPGA
```

>2 P_AAG81325 Human AFP protein sequence SEQ ID NO:168 - Homo sapiens. (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121

Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAG81325       1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR

DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ
                  *****
P_AAG81325     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAG81325    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc    181 PAAPPPYMPPQPSYPGA
                  *****
P_AAG81325    181 PAAPPPYMPPQPSYPGA
```

>3 P_AAY66735 Membrane-bound protein PRO1153 - Homo sapiens. (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121
Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAY66735      1 MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
P_AAY66735     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAY66735    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
DNA59842.nc    181 PAAPPPYMPPQPSYPGA
                  *****
P_AAY66735    181 PAAPPPYMPPQPSYPGA
                  *****
```

>4 P_AAB24074 Human PRO1153 protein sequence SEQ ID NO:49 - Homo sapiens. (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121
Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
P_AAB24074      1 MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
P_AAB24074     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
P_AAB24074    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
DNA59842.nc    181 PAAPPPYMPPQPSYPGA
                  *****
P_AAB24074    181 PAAPPPYMPPQPSYPGA
                  *****
```

>5 CAC38575.1 unnamed protein product - Homo sapiens (197 aa) [1 seg]

Score = 1118 (435 bits), Expect = e-121
Identities = 197/197 (100%), Positives = 197/197 (100%), at 1,1-197,197

```
DNA59842.nc      1 MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
CAC38575.1      1 MPPAGLRRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHR
                  *****
DNA59842.nc     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
CAC38575.1     61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFCLSCCCYLRRRQQ
                  *****
DNA59842.nc    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
CAC38575.1    121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN
                  *****
DNA59842.nc    181 PAAPPPYMPPQPSYPGA
                  *****
```

BLAST RESULTS B-2

CAC38575.1 181 PAAPPPYMPPQPSYPGA

>6 P_AAE06576 Human protein having hydrophobic domain, HP10764 - Homo (197 aa) [1 seg]

Score = 1114 (433 bits), Expect = e-121

Identities = 196/197 (99%), Positives = 197/197 (99%), at 1,1-197,197

DNA59842.nc 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR

P_AAE06576 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR

DNA59842.nc 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

P_AAE06576 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

DNA59842.nc 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN

P_AAE06576 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFIYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc 181 PAAPPPYMPPQPSYPGA

P_AAE06576 181 PAAPPPYMPPQPSYPGA

>7 CAC51150.1 unnamed protein product - Homo sapiens (197 aa) [1 seg]

Score = 1114 (433 bits), Expect = e-121

Identities = 196/197 (99%), Positives = 197/197 (99%), at 1,1-197,197

DNA59842.nc 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR

CAC51150.1 1 MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHR

DNA59842.nc 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

CAC51150.1 61 YCCRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQ

DNA59842.nc 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYN

CAC51150.1 121 LQSPFEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFIYPPSGPAPQYPLYPAGPPVYN

DNA59842.nc 181 PAAPPPYMPPQPSYPGA

CAC51150.1 181 PAAPPPYMPPQPSYPGA

BLAST RESULTS B-3